



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Seed, Brian et al.
- (ii) TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES AND METHODS
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Clark & Elbing LLP
(B) STREET: 585 Commercial Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02109-1024
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Patent in Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/756,018
(B) FILING DATE: 25-NOV-96
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/661,960
(B) FILING DATE: 12-JUN-1996
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/000,213
(B) FILING DATE: 14-JUN-1995
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Elbing, Karen Lech
(B) REGISTRATION NUMBER: 35,238
(C) REFERENCE/DOCKET NUMBER: 00786/284002
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617/723-6777
(B) TELEFAX: 617/723-8962
(C) TELEX:
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala Thr Glu Ala Gln Thr Thr Pro Pro Ala
1 5 10

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Thr Asn Ser Leu Glu Thr Ser Thr Gly Thr Ser Gly Pro Pro
1 5 10 15

Val Thr

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Leu Trp Asp Thr Trp Ala Asp Glu Ala Glu Lys Ala Leu Gly Pro
1 5 10 15

Leu Leu Ala Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp
20 25 30

Tyr Asp Phe Leu Pro Glu Thr Glu Pro Pro
35 40

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids

- (B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Asp Arg Arg Gln Ala Thr Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe
1 5 10 15

Leu Pro Glu Thr
20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Asp Arg Arg Gln Ala Thr Glu Phe Glu Phe Leu Asp Phe Asp Phe
1 5 10 15

Leu Pro Glu Thr
20

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Asp Arg Arg Gln Ala Ala Glu Tyr Glu Tyr Leu Asp Tyr Asp Phe
1 5 10 15

Leu Pro Glu Ala
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

00000" 00000" 00000"

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Arg Asp Arg Arg Gln Ala Ala Glu Phe Glu Phe Leu Asp Phe Asp Phe
 1 5 10 15
 Leu Pro Glu Ala
 20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2287 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AAGCTTACCA CCATGGACTG GACCTGGAGG TTCCTCTTCT TTGTGGTGGC AGCAGCTACA 60
 GGTGTCCAGT CCCAGGTGCA GCTGGTGCAG TCTGGGGCTG AGGTGAAGAA GCCTGGGTCC 120
 TCGGTGAAGG TCTCCTGCAA GGCTTCTGGA GGCACCTTCA GCAGCTATGC TATCAGCTGG 180
 GTGCGACAGG CCCCTGGACA AGGGCTTGAG TCGATGGGAG GGATCATCCC TATCTTTGGT 240
 ACAGCAAACCT ACGCACAGAA GTTCCAGGAC AGAGTCACGA TTACCGCGGA CGAATCCACG 300
 AGCACAGCCT ACATGGAGCT GAGCAGCCTG AGATCTGAGG ACACGGCCGT GTATTACTGT 360
 GCGAGAGATA ATGGAGCGTA TTGTAGTGGT GGTAGCTGCT ACTCGGGCTG GTTCGACCCC 420
 TGGGGCCAGG GAACCCTGGT CACCGTCTCT TCAGGTGAGT ACTGAATTCT AGCTTTCTGG 480
 GGCAGGCCAG GCCTGACCTT GGCTTTGGGG CAGGGAGGGG GCTAAGGTGA GGCAGGTGGC 540
 GCCAGCAGGT GCACACCCAA TGCCCATGAG CCCAGACACT GGACGCTGAA CCTCGCGGAC 600
 AGTTAAGAAC CCAGGGGCCT CTGCGCCTGG GCCCAGCTCT GTCCACACACC GCGGTCACAT 660
 GGCACCACCT CTCTTGCAGC CTCCACCAAG GGCCCATCGG TCTTCCCCCT GGCACCCTCC 720
 TCCAAGAGCA CCTCTGGGGG CACAGCGGCC CTGGGCTGCC TGGTCAAGGA CTACTTCCCC 780

03756018 032097

GAACCGGTGA CGGTGTCGTG GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCG	840
GCTGTCCTAC AGTCCTCAGG ACTCTACTCC CTCAGCAGCG TGGTGACCGT GCCCTCCAGC	900
AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA CACCAAGGTG	960
GACAAGAAAG TTGGTGAGAG GCCAGCACAG GGAGGGAGGG TGTCTGCTGG AAGCAGGCTC	1020
AGCGCTCCTG CCTGGACGCA TCCCGGCTAT GCAGCCCCAG TCCAGGGCAG CAAGGCAGGC	1080
CCCGTCTGCC TCTTCACCCG GAGCCTCTGC CCGCCCCACT CATGCTCAGG GAGAGGGTCT	1140
TCTGGCTTTT TCCCAGGCTC TGGGCAGGCA CAGGCTAGGT GCCCCTAACC CAGGCCCTGC	1200
ACACAAAGGG GCAGGTGCTG GGCTCAGACC TGCCAAGAGC CATATCCGGG AGGACCCTGC	1260
CCCTGACCTA AGCCCACCCC AAAGGCCAAA CTCTCCACTC CCTCAGCTCG GACACCTTCT	1320
CTCTCCCAG ATTCCAGTAA CTCCCAATCT TCTCTCTGCA GAGCCCAAAT CTTGTGACAA	1380
AACTCACACA TGCCCACCGT GCCCAGGTAA GCCAGCCGAG GCCTCGCCCT CCAGCTCAAG	1440
GCGGGACAGG TGCCCTAGAG TAGCCTGCAT CCAGGGACAG GCCCCAGCCG GGTGCTGACA	1500
CGTCCACCTC CATCTCTTCC TCAGCACCTG AACTCCTGGG GGGACCGTCA GTCTTCCTCT	1560
TCCCCCAA AACCAGGAC ACCCTCATGA TCTCCCGGAC CCCTGAGGTC ACATGCGTGG	1620
TGGTGGACGT GAGCCACGAA GACCCTGAGG TCAAGTTCAA CTGGTACGTG GACGGCGTGG	1680
AGGTGCATAA TGCCAAGACA AAGCCGCGGG AGGAGCAGTA CAACAGCACG TACCGGGTGG	1740
TCAGCGTCCT CACCGTCCTG CACCAGGACT GGCTGAATGG CAAGGAGTAC AAGTGCAAGG	1800
TCTCCAACAA AGCCCTCCCA GCCCCATCG AGAAACCAT CTCCAAAGCC AAAGGTGGGA	1860
CCCGTGGGGT GCGAGGGCCA CATGGACAGA GGCCGGCTCG GCCCACCCTC TGCCCTGAGA	1920
GTGACCGCTG TACCAACCTC TGTCCTACAG GGCAGCCCCG AGAACCACAG GTGTACACCC	1980
TGCCCCATC CCGGGATGAG CTGACCAAGA ACCAGGTCAG CCTGACCTGC CTGGTCAAAG	2040
GCTTCTATCC CAGCGACATC GCCGTGGAGT GGGAGAGCAA TGCGCAGCCG GAGAACAAC	2100
ACAAGACCAC GCCTCCCGTG CTGGACTCCG ACGGCTCCTT CTTCCTCTAC AGCAAGCTCA	2160
CCGTGGACAA GAGCAGGTGG CAGCAGGGGA ACGTCTTCTC ATGCTCCGTG ATGCATGAGG	2220
CTCTGCACAA CCACTACACG CAGAAGAGCC TCTCCCTGTC TCCGGTAAA TGAGTGCGAC	2280
GGCCGGC	2287

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Lys Leu Thr Thr Met Asp Trp Thr Trp Arg Phe Leu Phe Phe Val Val
1 5 10 15
Ala Ala Ala Thr Gly Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly
20 25 30
Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
35 40 45
Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala
50 55 60
Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly
65 70 75 80
Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala
85 90 95
Asp Glu Ser Thr Ala Arg Asp Asn Gly Ala Tyr Cys Ser Gly Gly Ser
100 105 110
Cys Tyr Ser Gly Trp Phe Asp Pro Trp Gly Gln Gly Thr Leu Val Thr
115 120 125
Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro
130 135 140
Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
145 150 155 160
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala
165 170 175
Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly
180 185 190
Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Asp Lys
195 200 205
Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys
210 215 220

Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 225 230 235 240

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
 245 250 255

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
 260 265 270

Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
 275 280 285

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
 290 295 300

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
 305 310 315 320

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
 325 330 335

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu
 340 345 350

Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
 355 360 365

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
 370 375 380

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 385 390 395 400

Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 405 410 415

Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 420 425 430

Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1894 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

0356018-032097

ATGGCGCTGT	CCTGGGTTCT	TACAGTCCTG	AGCCTCCTAC	CTCTGCTGGA	AGCCCAGATC	60
CCATTGTGTG	CCAACCTAGT	ACCGGTGCCC	ATCACCAACG	CCACCCTGGA	CCAGATCACT	120
GGCAAGTGGT	TTTATATCGC	ATCGGCCTTT	CGAAACGAGG	AGTACAATAA	GTCGGTTCAG	180
GAGATCCAAG	CAACCTTCTT	TTACTTCACC	CCCAACAAGA	CAGAGGACAC	GATCTTTCTC	240
AGAGAGTACC	AGACCCGACA	GGACCAGTGC	ATCTATAACA	CCACCTACCT	GAATGTCCAG	300
CGGGAAAATG	GGACCATCTC	CAGATACGTG	GGAGGCCAAG	AGCATTTTCG	TCACTTGCTG	360
ATCCTCAGGG	ACACCAAGAC	CTACATGCTT	GCTTTTGACG	TGAACGATGA	GAAGAACTGG	420
GGGCTGTCTG	TCTATGCTGA	CAAGCCAGAG	ACGACCAAGG	AGCAACTGGG	AGAGTTCTAC	480
GAAGCTCTCG	ACTGCTTGCG	CATTCCCAAG	TCAGATGTCT	TGTACACCGA	TTGGAAAAAG	540
GATAAGTGTG	AGCCACTGGA	GAAGCAGCAC	GAGAAGGAGA	GGAAACAGGA	GGAGGGGGAA	600
TCGGATCCCG	AGGGTGAGTA	CTAAGCTTCA	GCGCTCCTGC	CTGGACGCAT	CCCGGCTATG	660
CAGCCCCAGT	CCAGGGCAGC	AAGGCAGGCC	CCGTCTGCCT	CTTCACCCGG	AGCCTCTGCC	720
CGCCCCACTC	ATGCTCAGGG	AGAGGGTCTT	CTGGCTTTTT	CCCAGGCTCT	GGGCAGGCAC	780
AGGCTAGGTG	CCCCTAACCC	AGGCCCTGCA	CACAAAGGGG	CAGGTGCTGG	GCTCAGACCT	840
GCCAAGAGCC	ATATCCGGGA	GGACCCTGCC	CCTGACCTAA	GCCCACCCCA	AAGGCCAAAC	900
TCTCCACTCC	CTCAGCTCGG	ACACCTTCTC	TCCTCCCAGA	TTCCAGTAAC	TCCCAATCTT	960
CTCTCTGCAG	AGCCCAAATC	TTGTGACAAA	ACTCAGCAT	GCCCACCGTG	CCCAGGTAAG	1020
CCAGCCCAGG	CCTCGCCCTC	CAGCTCAAGG	CGGGACAGGT	GCCCTAGAGT	AGCCTGCATC	1080
CAGGGACAGG	CCCAGCCGG	GTGCTGACAC	GTCCACCTGC	ATCTCTTCTT	CAGCACCTGA	1140
ACTCCTGGGG	GGACCGTCAG	TCTTCCTCTT	CCCCCAAAA	CCCAAGGACA	CCCTCATGAT	1200
CTCCCGGACC	CCTGAGGTCA	CATGCGTGGT	GGTGGACGTG	AGCCACGAAG	ACCCTGAGGT	1260
CAAGTTCAAC	TGGTACGTGG	ACGGCGTGGA	GGTGCATAAT	GCCAAGACAA	AGCCGCGGGA	1320
GGAGCAGTAC	AACAGCACGT	ACCGGGTGGT	CAGCGTCCTC	ACCGTCCTGC	ACCAGGACTG	1380
GCTGAATGGC	AAGGAGTACA	AGTGCAAGGT	CTCCAACAAA	GCCCTCCCAG	CCCCCATCGA	1440
GAAAACCATC	TCCAAAGCCA	AAGGTGGGAC	CCGTGGGGTG	CGAGGGCCAC	ATGGACAGAG	1500
GCCGGCTCGG	CCCACCTCT	GCCCTGAGAG	TGACCGCTGT	ACCAACCTCT	GTCTTACAGG	1560
GCAGCCCCGA	GAACCACAGG	TGTACACCCT	GCCCCCATCC	CGGGATGAGC	TGACCAAGAA	1620

CCAGGTCAGC CTGACCTGCC TGGTCAAAGG CTTCTATCCC AGCGACATCG CCGTGGAGTG 1680
GGAGAGCAAT GGGCAGCCGG AGAACAACTA CAAGACCACG CCTCCCGTGC TGGACTCCGA 1740
CGGCTCCTTC TTCCTCTACA GCAAGCTCAC CGTGGACAAG AGCAGGTGGC AGCAGGGGAA 1800
CGTCTTCTCA TGCTCCGTGA TGCATGAGGC TCTGCACAAC CACTACACGC AGAAGAGCCT 1860
CTCCCTGTCT CCGGGTAAAT GAGTGCGACG GCCG 1894

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 437 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ala	Leu	Ser	Trp	Val	Leu	Thr	Val	Leu	Ser	Leu	Leu	Pro	Leu	Leu
1				5					10					15	
Glu	Ala	Gln	Ile	Pro	Leu	Cys	Ala	Asn	Leu	Val	Pro	Val	Pro	Ile	Thr
			20					25					30		
Asn	Ala	Thr	Leu	Asp	Gln	Ile	Thr	Gly	Lys	Trp	Phe	Tyr	Ile	Ala	Ser
			35					40				45			
Ala	Phe	Arg	Asn	Glu	Glu	Tyr	Asn	Lys	Ser	Val	Gln	Glu	Ile	Gln	Ala
	50					55					60				

Thr	Phe	Phe	Tyr	Phe	Thr	Pro	Asn	Lys	Thr	Glu	Asp	Thr	Ile	Phe	Leu	65	70	75	80
Arg	Glu	Tyr	Gln	Thr	Arg	Gln	Asp	Gln	Cys	Ile	Tyr	Asn	Thr	Thr	Tyr	85	90	95	
Leu	Asn	Val	Gln	Arg	Glu	Asn	Gly	Thr	Ile	Ser	Arg	Tyr	Val	Gly	Gly	100	105	110	
Gln	Glu	His	Phe	Ala	His	Leu	Leu	Ile	Leu	Arg	Asp	Thr	Lys	Thr	Tyr	115	120	125	
Met	Leu	Ala	Phe	Asp	Val	Asn	Asp	Glu	Lys	Asn	Trp	Gly	Leu	Ser	Val	130	135	140	
Tyr	Ala	Asp	Lys	Pro	Glu	Thr	Thr	Lys	Glu	Gln	Leu	Gly	Glu	Phe	Tyr	145	150	155	160
Glu	Ala	Leu	Asp	Cys	Leu	Arg	Ile	Pro	Lys	Ser	Asp	Val	Val	Tyr	Thr	165	170	175	
Asp	Trp	Lys	Lys	Asp	Lys	Cys	Glu	Pro	Leu	Glu	Lys	Gln	His	Glu	Lys	180	185	190	
Glu	Arg	Lys	Gln	Glu	Glu	Gly	Glu	Ser	Asp	Pro	Glu	Gly	Glu	Pro	Lys	195	200	205	
Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	210	215	220	
Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	225	230	235	240
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	245	250	255	
Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	260	265	270	
Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	275	280	285	
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	290	295	300	
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	305	310	315	320
Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	325	330	335	
Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	340	345	350	

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 355 360 365

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 370 375 380

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
 385 390 395 400

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
 405 410 415

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 420 425 430

Leu Ser Pro Gly Lys
 435

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 442 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Lys Leu Thr Thr Met Asp Trp Thr Trp Arg Phe Leu Phe Phe Val Val
 1 5 10 15

Ala Ala Ala Thr Gly Val Gln Ser Gln Val Gln Leu Val Gln Ser Gly
 20 25 30

Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala
 35 40 45

Ser Gly Gly Thr Phe Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala
 50 55 60

Pro Gly Gln Gly Leu Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly
 65 70 75 80

Thr Ala Asn Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala
 85 90 95

Asp Glu Ser Thr Ala Arg Asp Asn Gly Ala Tyr Cys Ser Gly Gly Ser
 100 105 110

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Cys Tyr Ser Gly Trp Phe Asp	Pro Trp Gly Gln Gly Thr Leu Val Thr
115	120 125
Val Ser Ser Ala Ser Thr Lys	Gly Pro Ser Val Phe Pro Leu Ala Pro
130	135 140
Ser Ser Lys Ser Thr Ser Gly	Gly Thr Ala Ala Leu Gly Cys Leu Val
145	150 155 160
Lys Asp Tyr Phe Pro Glu Pro Val	Thr Val Ser Trp Asn Ser Gly Ala
	165 170 175
Leu Thr Ser Gly Val His Thr Phe	Pro Ala Val Leu Gln Ser Ser Gly
	180 185 190
Leu Tyr Ser Leu Ser Ser Val Val	Thr Val Pro Ser Ser Ser Asp Lys
	195 200 205
Lys Val Glu Pro Lys Ser Cys Asp	Lys Thr His Thr Cys Pro Pro Cys
	210 215 220
Pro Ala Pro Glu Leu Leu Gly Gly	Pro Ser Val Phe Leu Phe Pro Pro
	225 230 235 240
Lys Pro Lys Asp Thr Leu Met Ile Ser	Arg Thr Pro Glu Val Thr Cys
	245 250 255
Val Val Val Asp Val Ser His Glu Asp	Pro Glu Val Asn Phe Ser Trp
	260 265 270
Tyr Val Asp Gly Val Glu Val His Asn	Asn Lys Thr Lys Pro Arg Glu
	275 280 285
Glu Asn Tyr Ser Ser Thr Tyr Arg	Val Val Ser Val Leu Thr Val Leu
	290 295 300
His Gln Asp Trp Leu Asn Gly Lys	Glu Tyr Lys Cys Asn Val Ser Asn
	305 310 315 320
Lys Ala Leu Pro Ala Pro Ile Glu	Lys Asn Ile Ser Lys Ala Lys Gly
	325 330 335
Gln Pro Arg Glu Pro Gln Val Tyr Thr	Leu Pro Pro Ser Arg Asp Glu
	340 345 350
Leu Thr Lys Asn Gln Val Ser Leu Thr	Cys Leu Val Lys Gly Phe Tyr
	355 360 365
Pro Ser Asp Ile Ala Val Glu Trp	Glu Ser Asn Gly Gln Pro Glu Asn
	370 375 380

Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
 385 390 395 400
 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
 405 410 415
 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
 420 425 430
 Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
 435 440

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Glu Met Leu Arg Asn Ser Thr Asp Thr Thr Pro Leu Thr Gly
 1 5 10 15
 Pro Gly Thr Pro Glu Ser Thr Thr Val Glu Pro Ala Ala Arg Arg Ser
 20 25 30
 Thr Gly Leu Asp Ala Gly Gly Ala Val Thr Glu
 35 40

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Leu Thr Thr Glu Leu Ala Asn Met Gly Asn Leu Ser Thr Asp Ser Ala
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acids
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Thr Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser
1 5 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acids
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Asp Tyr Glu Tyr Asp Glu Leu Pro
1 5

260250" 8T095280